

## REMARKS

### 1. Status of the Claims and Formal Matters

#### a. Amendments

Claims 1-20 are pending in this application. Claims 1-20 are hereby cancelled without prejudice to pursuing these claims in a continuing application. Claims 21-31 are new. Upon entry of these amendments, claims 21-31 are pending and under active consideration. Applicants respectfully request entry of the amendments and remarks made herein into the file history of the present application.

New claim 21 recites a nucleic acid consisting of 18 to 120 nucleotides, support for which may be found throughout the application including claim 1 as originally filed. New claim 21 also recites that the sequence of the nucleic acid may comprise (a) at least 18 consecutive nucleotides of SEQ ID NOS: 861, 862, or 863, support for which may be found throughout the application including at SEQ ID NOS: 861, 862, and 863, and claim 1 as originally filed; (b) an RNA equivalent of (a), support for which may be found throughout the application including at claim 1 as originally filed; (c) a sequence at least 62/87 identical to (a) or (b), support for which may be found at claim 1 as originally filed and at Table 1, which shows that (i) the sequence of SEQ ID NO: 863, of which the first half is a partial inverse of its second half, is 87 nucleotides in length; and (ii) within the predicted hairpin formed by the nucleic acid of SEQ ID NO: 863, 62 complementary nucleotides are paired; or (d) the complement of any one of (a)-(c), support for which may be found at Table 1 and ¶ 17 of the application as originally filed.

New claim 22 recites a nucleic acid comprising the sequence of SEQ ID NO: 3588, support for which can be found at Table 1 and claim 1 as originally filed.

New claim 23 recites a nucleic acid with a sequence consisting of (a) SEQ ID NOS: 861, 862, or 863; (b) an RNA equivalent of (a); (c) a sequence at least 62/87 identical to (a) or (b); or (d) the complement of any one of (a)-(c), support for which may be found throughout the application including at new claim 21.

New claim 24 recites that the nucleic acid of claim 21 consists of 18 to 24 nucleotides, support for which may be found at claim 1 as originally filed.

New claim 25 recites that the nucleic acid of claim 1 is an RNA, support for which may be found throughout the application including at claim 1 as originally filed.

New claim 26 recites that the nucleic acid of claim 24 is capable of modulating expression of a target gene, support for which may be found at claim 1 as originally filed.

New claim 27 recites that the nucleic acid of 26 is (a) at least 15/21 complementary to a binding site sequence of 18 to 24 nucleotides of a target gene, support for which can be found at claim 1 as originally filed and at Table 2, which shows that among all listed target binding sites of the nucleotide represented by SEQ ID NO: 3588, the sequence of which is included in the sequence of SEQ ID NO: 863, at the lowest level of complementarity a target binding site of 21 nucleotides has 15 nucleotides complementary to the sequence of SEQ ID NO: 3588; and (b) that the binding site sequence is located in an untranslated region of RNA encoded by the target gene, support for which can be found at claim 1 and ¶ 22 of the specification as originally filed.

New claim 28 recites a vector comprising an HCMV nucleic acid wherein the HCMV nucleic acid consists of the nucleic acid of claim 21, support for which can be found at ¶ 24 of the application as originally filed.

New claim 29 recites a probe comprising an HCMV nucleic acid, wherein the HCMV nucleic acid consists of the nucleic acid of claim 21, support for which can be found at ¶ 28 of the application as originally filed.

New claim 30 recites a gene expression inhibition system comprising the vector of claim 28 and a means for inserting said vector into a cell, support for which can be found at ¶¶ 25-27 of the application as originally filed.

New claim 31 recites a gene expression detection system comprising the probe of claim 29 and a gene expression detector functional to selectively detect expression of at least one gene, support for which can be found at ¶¶ 29-30 of the application as originally filed.

## **b. Election**

### **(1) Groups I-IX**

At pages 2-4 of the Office Action, the Examiner requires restriction to one of the following inventions under 35 U.S.C. 121:

- I. Claims 1-8, 11, 12 drawn to a bioinformatically detectable viral gene and a vector comprising the gene, probes, etc.
- II. Claims 9-10, drawn to a method of inhibiting translation using a vector.
- III. Claim 13, drawn to a method of detecting expression using a probe.

- IV. Claim 14, drawn to a composition comprising a probe and “a gene expression detector.”
- V. Claim 15, drawn to an unspecified uncharacterized antiviral substance “capable of neutralizing RNA.”
- VI. Claim 16, drawn to an antiviral substance which is RNA.
- VII. Claim 17, drawn to an antiviral substance which “comprises immunologically neutralizing.”
- VIII. Claims 18-19, drawn to methods of antiviral treatment by neutralizing RNA.
- IX. Claim 20, drawn to methods of antiviral treatment by “immunologically neutralizing.”

Applicant elect without traverse Group I, which now is considered claims 21-31, drawn to a nucleic acids related to a bioinformatically detectable viral gene and a vector comprising the gene, probes, etc.

## **(2) Single Nucleic Acid Sequence**

At page 3 of the Office Action, the Examiner requires restriction to a single nucleic acid sequence under MPEP 803.04. Applicant elects with traverse nucleic acids related to SEQ ID NO: 863 for further prosecution.

### **(a) Traversal – Up to Ten Nucleic Acid Sequences Reasonable**

The Examiner is permitted under 35 U.S.C. 121 to issue a restriction requirement between independent and distinct inventions. However, the Director has partially waived the requirements of 37 C.F.R. § 1.141 *et seq.* to permit a reasonable number of nucleotide sequences to be claimed in a single application. *See Examination of Patent Applications Containing Nucleotide Sequence*, 1192 O.G. 68 (November 19, 1996). It has been determined that normally **ten** sequences constitute a reasonable number for examination purposes absent an exceptional case. *See MPEP 803.04.*

The Examiner has failed to demonstrate that the claimed sequences are an exceptional case necessitating that the number of sequences to be selected be less than ten. Applicant respectfully submits that the Examiner is impermissibly disregarding the waiver of 37 C.F.R. § 1.141 *et seq.* Accordingly, Applicant respectfully requests reconsideration of the restriction requirement and the opportunity to elect ten sequences for further prosecution.

**(b) Traversal – SEQ ID NOS: 861, 862 and 863 are Related**

Notwithstanding the remarks above, Applicant respectfully requests that SEQ ID NOS: 861 and 862 be examined along with SEQ ID NO: 863. SEQ ID NO: 863 is a hairpin which is located on the plus strand of HCMV at position 27642-27709 (Accession X17403.1) at an intergenic location between viral genes UL22A and UL23. The hairpins comprising the sequences of SEQ ID NOS: 861 and 862 are clustered with the hairpin comprising the sequence of SEQ ID NO: 863 within an approximate 2,400 nucleotide region of the HCMV genome. In view of SEQ ID NOS: 861, 862 and 863 being related by genomic location, Applicant respectfully requests that SEQ ID NOS: 861 and 862 be examined along with SEQ ID NO: 863.

**(3) Single Host Target Sequence**

At page 4 of the Office Action, the Examiner requires election of a single host target gene. Applicant without traverse elects host target gene NBS1, which has the sequence of SEQ ID NO: 34436.

**2. Conclusion**

Applicant respectfully submits that the instant application is in good and proper order for allowance and early notification to this effect is solicited. If, in the opinion of the Examiner, a telephone conference would expedite prosecution of the instant application, the Examiner is encouraged to call the undersigned at the number listed below.

Respectfully submitted,

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Dated: August 16, 2006

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